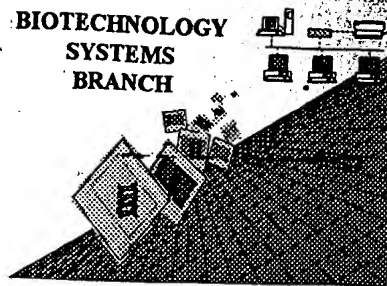


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



0270

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/684,026

Source: O/PE

Date Processed by STIC: 10/19/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

BEST AVAILABLE COPY

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/684,026

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) ____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

Does Not Comply
Corrected Diskette Needed

RAW SEQUENCE LISTING DATE: 10/19/2000
PATENT APPLICATION: US/09/684,026 TIME: 11:48:39

Input Set : A:\11076-002001 Sequence Listing.txt
Output Set: N:\CRF3\10192000\I684026.raw

pp 1,3

OK

4 <110> APPLICANT: Devico, Anthony Louis
5 Fouts, Timothy R.
6 Tuskan, Robert G.
8 <120> TITLE OF INVENTION: VIRUS COAT PROTEIN/RECEPTOR CHIMERAS AND
9 METHODS OF USE
11 <130> FILE REFERENCE: 11076-002001
13 <140> CURRENT APPLICATION NUMBER: US/09/684,026
13 <141> CURRENT FILING DATE: 2000-10-06
13 <150> PRIOR APPLICATION NUMBER: 60/158,321
14 <151> PRIOR FILING DATE: 1999-10-08
16 <160> NUMBER OF SEQ ID NOS: 10
18 <170> SOFTWARE: FastSEQ for Windows Version 4.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 10
22 <212> TYPE: PRT
23 <213> ORGANISM: Artificial Sequence
25 <220> FEATURE:
26 <223> OTHER INFORMATION: Artificial Sequence - polypeptide
28 <400> SEQUENCE: 1
29 Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
30 1 5 10
32 <210> SEQ ID NO: 2
33 <211> LENGTH: 39
34 <212> TYPE: DNA
35 <213> ORGANISM: Artificial Sequence
37 <220> FEATURE:
38 <223> OTHER INFORMATION: Artificial Sequence - primer
40 <400> SEQUENCE: 2
41 gggggtacca tgcccatggg gtctctgcaa ccgctggcc 39
43 <210> SEQ ID NO: 3
44 <211> LENGTH: 66
45 <212> TYPE: DNA
46 <213> ORGANISM: Artificial Sequence
48 <220> FEATURE:
49 <223> OTHER INFORMATION: Artificial Sequence - primer
51 <400> SEQUENCE: 3
52 ggggtccggag cccgagccac cgccaccaga ggatccacgc ttctcgcgct gcaccacgcg 60
53 gcgctt 66
55 <210> SEQ ID NO: 4
56 <211> LENGTH: 69
57 <212> TYPE: DNA
58 <213> ORGANISM: Artificial Sequence
60 <220> FEATURE:
61 <223> OTHER INFORMATION: Artificial Sequence - primer
63 <400> SEQUENCE: 4
64 ggggtccggag gaggtgggtc ggggtggcgc gcggccgcta agaaagtggg gctgggcaaa 60
65 aaaggggat 69

invalid - give source of genetic material -
see circled portion of
item 12 on Error
summary sheet

DATE: 10/19/2000

TIME: 11:48:39

Input Set : A:\11076-002001 Sequence Listing.txt

Output Set: N:\CRF3\10192000\I684026.raw

```

67 <210> SEQ ID NO: 5
68 <211> LENGTH: 77
69 <212> TYPE: DNA
70 <213> ORGANISM: Artificial Sequence
72 <220> FEATURE:
73 <223> OTHER INFORMATION: Artificial Sequence - primer
75 <400> SEQUENCE: 5
76 ggggttttaaa cttattacag atcctcttct gagatgagtt tttgttcagc tagcaccacg 60
77 atgtctattt tgaactc 77
80 <210> SEQ ID NO: 6
81 <211> LENGTH: 111
82 <212> TYPE: DNA
83 <213> ORGANISM: Artificial Sequence
84 <220> FEATURE:
85 <223> OTHER INFORMATION: Artificial Sequence - primer
87 <400> SEQUENCE: 6
88 gggggtacca tgcacatggg gtctctgcaa ccgtggcca ccttgtagct gctggggatg 60
89 ctggctgctt cctgcctcgg aaagaacgtg accgagaact tcaacatgtg g 111
91 <210> SEQ ID NO: 7
92 <211> LENGTH: 39
93 <212> TYPE: DNA
94 <213> ORGANISM: Artificial Sequence
96 <220> FEATURE:
97 <223> OTHER INFORMATION: Artificial Sequence - primer
99 <400> SEQUENCE: 7
100 ggggggatccg atcttcacca ccttgatctt gtacagctc 39
102 <210> SEQ ID NO: 8
103 <211> LENGTH: 75
104 <212> TYPE: DNA
105 <213> ORGANISM: Artificial Sequence
107 <220> FEATURE:
108 <223> OTHER INFORMATION: Artificial Sequence - primer
110 <400> SEQUENCE: 8
111 ctgtgcgtga cctggggcgc gggcgagatg aagaactgca gcttcaacat cggcgcgggc 60
112 cgcctgatca gctgc 75
114 <210> SEQ ID NO: 9
115 <211> LENGTH: 75
116 <212> TYPE: DNA
117 <213> ORGANISM: Artificial Sequence
119 <220> FEATURE:
120 <223> OTHER INFORMATION: Artificial Sequence - primer
122 <400> SEQUENCE: 9
123 gcagctgac aggcggcccg cgccgatgtt gaagctgcag ttcttcatct cgcccgcgcc 60
124 cagggtcacg cacag 75
126 <210> SEQ ID NO: 10
127 <211> LENGTH: 21
128 <212> TYPE: PRT
129 <213> ORGANISM: Artificial Sequence
131 <220> FEATURE:

```

RAW SEQUENCE LISTING

DATE: 10/19/2000

PATENT APPLICATION: US/09/684,026

TIME: 11:48:39

Input Set : A:\11076-002001 Sequence Listing.txt

Output Set: N:\CRF3\10192000\I684026.raw

132 <223> OTHER INFORMATION: Artifical Sequence amino acid
134 <400> SEQUENCE: 10
135 Gly Ser Ser Gly Gly Gly Gly Ser Gly Ser Gly Gly Gly Ser Gly
136 1 5 10 15
137 Gly Gly Ala Ala Ala
138 20

invalid - give source

VERIFICATION SUMMARY

DATE: 10/19/2000

PATENT APPLICATION: US/09/684,026

TIME: 11:48:40

Input Set : A:\11076-002001 Sequence Listing.txt

Output Set: N:\CRF3\10192000\I684026.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date